SEQUENCE LISTING

<110> HINUMA, Shuji
KAWAMATA, Yuji
FUJII, Ryo
MATSUMOTO, Hirokazu

<120> Prolactin Secretion Modulator

<130> 2472US0P

<140> US 09/446,543
<141> 1999-12-20

<150> PCT/JP98/02765
<151> 1998-06-22

<150> JP 9-165437
<151> 1997-06-23

<160> 99

B1

<170> PatentIn version 3.0

<210> 1
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<400> 1

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Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg
        35                  40                  45

Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Pro Gly Asp Gly Pro
    50                  55                  60

Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly
65                  70                  75                  80
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tggtacgcrg gccgtgggat ccggcccgtg ggccgcttcg gccggcgaag agctgcccyg
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ggggacggac ccaggcctgg cccccggcgt gtgccggcct gcttccgcct ggaaggcggy
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<220>
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20 25 30

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1 5 10 15

Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
20 25 30

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Val Gly Arg Phe
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Val Gly Arg Phe Gly
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<212> DNA
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<211> 63
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<210> 18
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<212> DNA
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<213> Human

<400> 19

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Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
35 40 45

Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr
50 55 60

Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
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Val Val Leu Val His Pro Leu Arg Arg Arg Ile
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<210> 20
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<212> PRT
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<400> 20

Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu
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Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly
20 25 30

Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg
35 40 45

Thr Phe Cys Leu Leu Val Val Val Val Val
50 55

B1 cont

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<400> 21

Met Ala Ser Ser Thr Thr Arg Gly Pro Arg Val Ser Asp Leu Phe Ser
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Gly Leu Pro Pro Ala Val Thr Thr Pro Ala Asn Gln Ser Ala Glu Ala
20 25 30

Ser Ala Gly Asn Gly Ser Val Ala Gly Ala Asp Ala Pro Ala Val Thr
35 40 45

Pro Phe Gln Ser Leu Gln Leu Val His Gln Leu Lys Gly Leu Ile Val
50 55 60

Leu Leu Tyr Ser Val Val Val Val Val Gly Leu Val Gly Asn Cys Leu
65 70 75 80

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Leu Val Leu Val Ile Ala Arg Val Arg Arg Leu His Asn Val Thr Asn
                85                  90                  95

Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu Met Cys Thr Ala
            100                 105                 110

Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
        115                 120                 125

Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Pro Val Thr
    130                 135                 140

Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
145                 150                 155                 160

Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser
                165                 170                 175

Ala Tyr Ala Val Leu Ala Ile Trp Ala Leu Ser Ala Val Leu Ala Leu
            180                 185                 190

Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
        195                 200                 205

Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu
    210                 215                 220

Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
225                 230                 235                 240

Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val
                245                 250                 255

Val Pro Gly Cys Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
            260                 265                 270

Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val Phe Ala
        275                 280                 285

Val Cys Trp Leu Pro Leu His Val Phe Asn Leu Leu Arg Asp Leu Asp
    290                 295                 300

Pro His Ala Ile Asp Pro Tyr Ala Phe Gly Leu Val Gln Leu Leu Cys
305                 310                 315                 320
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His Trp Leu Ala Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala
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Trp Leu His Asp Ser Phe Arg Glu Glu Leu Arg Lys Leu Leu Val Ala
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Val Ile
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20 25 30

Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly Trp Val
35 40 45

Phe Gly Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Ala Val Thr
50 55 60

Val Tyr Val Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr
65 70 75 80

Val Val Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser
85 90 95

Ala Tyr Ala Val Leu Ala Ile Trp Val Leu Ser Ala Val Leu Ala Leu
100 105 110

Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
115 120 125

Arg Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Leu
130 135 140

Tyr Ala Trp Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val
145 150 155 160

Ile Leu Leu Ser Tyr Ala Arg Val Ser Val Lys Leu Arg Asn Arg Val
165 170 175

Val Pro Gly Arg Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
180 185 190

Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Val
195 200 205

<210> 23
<211> 126
<212> PRT
<213> murine

<400> 23

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Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser Ala Val Leu Ala Leu
20 25 30

Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro His Asp Val
35 40 45

Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln Ile
50 55 60

Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala
65 70 75 80

Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val
85 90 95

Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg
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120

gccttcgagc cacgcggctg ggtgttcggc ggcggcctgt gccacctggt cttcttcctg
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cagccggtca ccgtctatgt gtcggtgttc acgctcacca ccatcgcagt ggaccggtac
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273

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<211> 177
<212> DNA
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120

ggcgcggacg ctccagccgt cacgcccttc cagagcctgc agctggtgca tcagctgaag
180

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240

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300

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gccttcgagc cacgcggctg ggtgttcggc ggcggcctgt gccacctggt cttcttcctg
420

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600

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gtgacccaga gccaggccga ctgggaccgc gctcggcgcc ggcgcacctt ctgcttgctg
840

gtggtggtcg tggtggtgtt cgccgtctgc tggctgccgc tgcacgtctt caacctgctg
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cgggacctcg acccccacgc catcgaccct tacgcctttg ggctggtgca gctgctctgc
960

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1020

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<211> 618
<212> DNA
<213> murine

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gccttcgagc cacgcggctg ggtgttcggc ggcggcctgt gccacctggt cttcttcctg
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caggcggtca ccgtctatgt gtcggtgttc acgctcacca ccatcgcagt ggaccgctac
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gtcgtgctgg tgcacccgct gaggcggcgc atctcgctgc gcctcagcgc ctacgctgtg
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ctggccatct gggtgctgtc cgcggtgctg gcgctgcccg ccgccgtgca cacctatcac
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gtggagctca agccgcacga cgtgcgcctc tgcgaggagt tctggggctc ccaggagcgc
420

cagcgccagc tctacgcctg ggggctgctg ctggtcacct acctgctccc tctgctggtc
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618

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<211> 378
<212> DNA
<213> murine

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caacgccaga tctacgcctg ggggctgctt ctgggcacct atttgctccc cctgctggcc
240

atcctcctgt cttacgtacg ggtgtcagtg aagctgagga accgcgtggt gcctggcagc
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<213> artificial

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<223> any base (A, G, C, T)

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<220>
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<212> DNA
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<220>
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<210> 34
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<212> DNA
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aacaccgaca catagacggt gacc
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<210> 35
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<222> (18)..(18)
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<210> 37
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<210> 39
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<212> DNA
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<220>
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<400> 42
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<210> 43
<211> 24
<212> DNA
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<400> 43
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<210> 44
<211> 98
<212> PRT
<213> bovine

<400> 44

Met Lys Ala Val Gly Ala Trp Leu Leu Cys Leu Leu Leu Leu Gly Leu
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20 25 30

Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly Arg Gly Ile Arg
35 40 45

Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Ala Leu Gly Asp Gly Pro
50 55 60

Arg Pro Gly Pro Arg Arg Val Pro Ala Cys Phe Arg Leu Glu Gly Gly

65 70 75 80

Ala Glu Pro Ser Arg Ala Leu Pro Gly Arg Leu Thr Ala Gln Leu Val
85 90 95

Gln Glu

<210> 45
<211> 83
<212> PRT
<213> rat

<400> 45

Met Ala Leu Lys Thr Trp Leu Leu Cys Leu Leu Leu Leu Ser Leu Val
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Leu Pro Gly Ala Ser Ser Arg Ala His Gln His Ser Met Glu Thr Arg
20 25 30

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
35 40 45

Val Gly Arg Phe Gly Arg Arg Arg Ala Thr Pro Arg Asp Val Thr Gly
50 55 60

Leu Gly Gln Leu Ser Cys Leu Pro Leu Asp Gly Arg Thr Lys Phe Ser
65 70 75 80

Gln Arg Gly

<210> 46
<211> 249
<212> DNA
<213> rat

<400> 46
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120

tacacgggcc gcgggatcag gcctgtgggc cgcttcggca ggagaagggc aaccccgagg

180

gatgtcactg gacttggcca actcagctgc ctcccactgg atggacgcac caagttctct
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cagcgtgga
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<223> rat fragment (22-52)

<400> 47

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20 25 30

B1
wf

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<211> 32
<212> PRT
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<220>
<223> rat fragment (22-53)

<400> 48

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Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
20 25 30

<210> 49
<211> 33
<212> PRT
<213> artificial

<220>
<223> rat fragment (22-54)

<400> 49

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1 5 10 15

Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
20 25 30

Arg

<210> 50
<211> 20
<212> PRT
<213> artificial

<220>
<223> rat fragment (33-53)

<400> 50

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1 5 10 15

Val Gly Arg Phe
20

<210> 51
<211> 21
<212> PRT
<213> artificial

<220>
<223> rat fragment (33-53)

<400> 51

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
1 5 10 15

Val Gly Arg Phe Gly
20

<210> 52
<211> 22
<212> PRT
<213> artificial

<220>
<223> rat fragment (33-54)

<400> 52

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Thr Gly Arg Gly Ile Arg Pro
1 5 10 15

Val Gly Arg Phe Gly Arg
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<210> 53
<211> 93
<212> DNA
<213> rat

<400> 53
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B1 Cont

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<212> DNA
<213> rat

<400> 54
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60

acgggccgcg ggatcaggcc tgtgggccgc ttcggc
96

<210> 55
<211> 99
<212> DNA
<213> rat

<400> 55
agccgagccc accagcactc catggagaca agaacccctg atatcaatcc tgcctggtac
60

acgggccgcg ggatcaggcc tgtgggccgc ttcggcagg
99

<210> 56
<211> 60
<212> DNA
<213> rat

<400> 56
acccctgata tcaatcctgc ctggtacacg ggccgcggga tcaggcctgt gggccgcttc
60

<210> 57
<211> 63
<212> DNA
<213> rat

<400> 57
acccctgata tcaatcctgc ctggtacacg ggccgcggga tcaggcctgt gggccgcttc
60

ggc
63

<210> 58
<211> 66
<212> DNA
<213> rat

<400> 58
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60

ggcagg
66

<210> 59

<211> 87
<212> PRT
<213> human

<400> 59

Met Lys Val Leu Arg Ala Trp Leu Leu Cys Leu Leu Met Leu Gly Leu
1 5 10 15

Ala Leu Arg Gly Ala Ala Ser Arg Thr His Arg His Ser Met Glu Ile
20 25 30

Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg
35 40 45

Pro Val Gly Arg Phe Gly Arg Arg Arg Ala Thr Leu Gly Asp Val Pro
50 55 60

Lys Pro Gly Leu Arg Pro Arg Leu Thr Cys Phe Pro Leu Glu Gly Gly
65 70 75 80

Ala Met Ser Ser Gln Asp Gly
85

<210> 60
<211> 261
<212> DNA
<213> human

<400> 60
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60

gctgcaagtc gtacccatcg gcactccatg gagatccgca cccctgacat caatcctgcc
120

tggtacgcca gtcgcgggat caggcctgtg ggccgcttcg gtcggaggag ggcaaccctg
180

ggggacgtcc ccaagcctgg cctgcgaccc cggctgacct gcttcccccc ggaaggcggt
240

gctatgtcgt cccaggatgg c
261

<210> 61
<211> 31
<212> PRT
<213> artificial

<220>
<223> human fragment (23-53)

<400> 61

Ser Arg Thr His Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn
1 5 10 15

Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe
20 25 30

<210> 62
<211> 32
<212> PRT
<213> artificial

<220>
<223> human fragment (23-54)

<400> 62

Ser Arg Thr His Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn
1 5 10 15

Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe Gly
20 25 30

<210> 63
<211> 32
<212> PRT
<213> artificial

<220>
<223> human fragment (23-55)

<400> 63

Ser Arg Thr His Arg His Ser Met Glu Ile Arg Thr Pro Asp Ile Asn
1 5 10 15

Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro Val Gly Arg Phe Gly

20 25 30

<210> 64
<211> 20
<212> PRT
<213> artificial

<220>
<223> human fragment (34-53)

<400> 64

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro
1 5 10 15

Val Gly Arg Phe
20

<210> 65
<211> 21
<212> PRT
<213> artificial

<220>
<223> human fragment (34-54)

<400> 65

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro
1 5 10 15

Val Gly Arg Phe Gly
20

<210> 66
<211> 22
<212> PRT
<213> artificial

<220>
<223> human fragment (34-55)

<400> 66

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Ser Arg Gly Ile Arg Pro
1 5 10 15

Val Gly Arg Phe Gly Arg
20

<210> 67
<211> 93
<212> DNA
<213> human

<400> 67
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60

gccagtcgcg ggatcaggcc tgtgggccgc ttc
93

<210> 68
<211> 96
<212> DNA
<213> human

<400> 68
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60

gccagtcgcg ggatcaggcc tgtgggccgc ttcggt
96

<210> 69
<211> 99
<212> DNA
<213> human

<400> 69
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60

gccagtcgcg ggatcaggcc tgtgggccgc ttcggtcgg
99

<210> 70
<211> 60
<212> DNA

<213> human

<400> 70
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60

<210> 71
<211> 63
<212> DNA
<213> human

<400> 71
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60

ggt
63

<210> 72
<211> 66
<212> DNA
<213> human

<400> 72
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60

ggtcgg
66

<210> 73
<211> 22
<212> PRT
<213> artificial

<220>
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<220>
<221> PEPTIDE
<222> (22)..(22)
<223> Absent or Arg when aa21 is Gly

<220>
<221> PEPTIDE
<222> (21)..(21)
<223> Absent or Gly

<220>
<221> PEPTIDE
<222> (11)..(11)
<223> Gly or Ser

<220>
<221> PEPTIDE
<222> (10)..(10)
<223> Ala or Thr

<400> 73

Thr Pro Asp Ile Asn Pro Ala Trp Tyr Xaa Xaa Arg Gly Ile Arg Pro
1 5 10 15

Val Gly Arg Phe Xaa Xaa
20

B1 Cont

<210> 74
<211> 11
<212> PRT
<213> artificial

<220>
<223> ligand polypeptide

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<221> PEPTIDE
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<223> Ile or Thr

<220>
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<222> (5)..(5)
<223> Gln or Arg

<220>
<221> PEPTIDE
<222> (3)..(3)
<223> Ala or Thr

<400> 74

Ser Arg Xaa His Xaa His Ser Met Glu Xaa Arg
1 5 10

<210> 75
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<212> DNA
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<220>
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<400> 75
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26

<210> 76
<211> 24
<212> DNA
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<220>
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<400> 76
taccaggcag gattgataca gggg
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<210> 77
<211> 25
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<220>
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<400> 77
ggcatcatcc aggaagacgg agcat
25

<210> 78
<211> 25
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<220>
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<400> 78
agcagaggag agggagggta gagga
25

<210> 79
<211> 22
<212> DNA
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<220>
<223> primer

<400> 79
acgtggcttc tgtgcttgct gc
22

<210> 80
<211> 25
<212> DNA
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<220>
<223> primer

<400> 80
gcctgatccc gcggcccgtg tacca
25

<210> 81
<211> 26

<212> DNA
<213> artificial

<220>
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<400> 81
ttgcccttct cctgccgaag cggccc
26

<210> 82
<211> 27
<212> DNA
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<220>
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<400> 82
ggcgggggct gcaagtcgta cccatcg
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<210> 83
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<210> 84
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<220>
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<400> 84

caggcaggat tgatgtcagg ggtgcgg
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<210> 85
<211> 27
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<220>
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<400> 85
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<210> 86
<211> 27
<212> DNA
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<220>
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<400> 86
ggcctcctcg gaggagccaa gggatga
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<210> 87
<211> 27
<212> DNA
<213> artificial

<220>
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<400> 87
gggaaaggag cccgaaggag aggagag
27

<210> 88
<211> 25
<212> DNA

<213> artificial

<220>
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<400> 88
cctgctggcc attctcctgt cttac
25

<210> 89
<211> 25
<212> DNA
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<220>
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<400> 89
gggtccaggt cccgcagaag gttga
25

<210> 90
<211> 25
<212> DNA
<213> artificial

<220>
<223> primer

<400> 90
gaagacggag catggccctg aagac
25

<210> 91
<211> 25
<212> DNA
<213> artificial

<220>
<223> primer

<400> 91
ggcagctgag ttggccaagt ccagt

25

<210> 92
<211> 15
<212> PRT
<213> artificial

<220>
<223> N-terminal peptide

<400> 92

Cys Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe
1 5 10 15

<210> 93
<211> 15
<212> PRT
<213> artificial

<220>
<223> C-terminal peptide

<400> 93

Cys Ala Trp Tyr Ala Gly Arg Gly Ile Arg Pro Val Gly Arg Phe
1 5 10 15

<210> 94
<211> 15
<212> PRT
<213> artificial

<220>
<223> central peptide

<400> 94

Cys Glu Ile Arg Thr Pro Asp Ile Asn Pro Ala Trp Tyr Ala Gly
1 5 10 15

<210> 95
<211> 30
<212> DNA
<213> artificial

<220>
<223> primer

<400> 95
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30

<210> 96
<211> 31
<212> DNA
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<220>
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<400> 96
gctgactcga cagcactgtc ttctcgagct g
31

<210> 97
<211> 21
<212> DNA
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<220>
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21

<210> 98
<211> 20
<212> DNA
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<220>
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<400> 98
atattctggc catgaggcac
20

<210> 99
<211> 28
<212> DNA
<213> artificial

<220>
<223> primer

<400> 99
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28